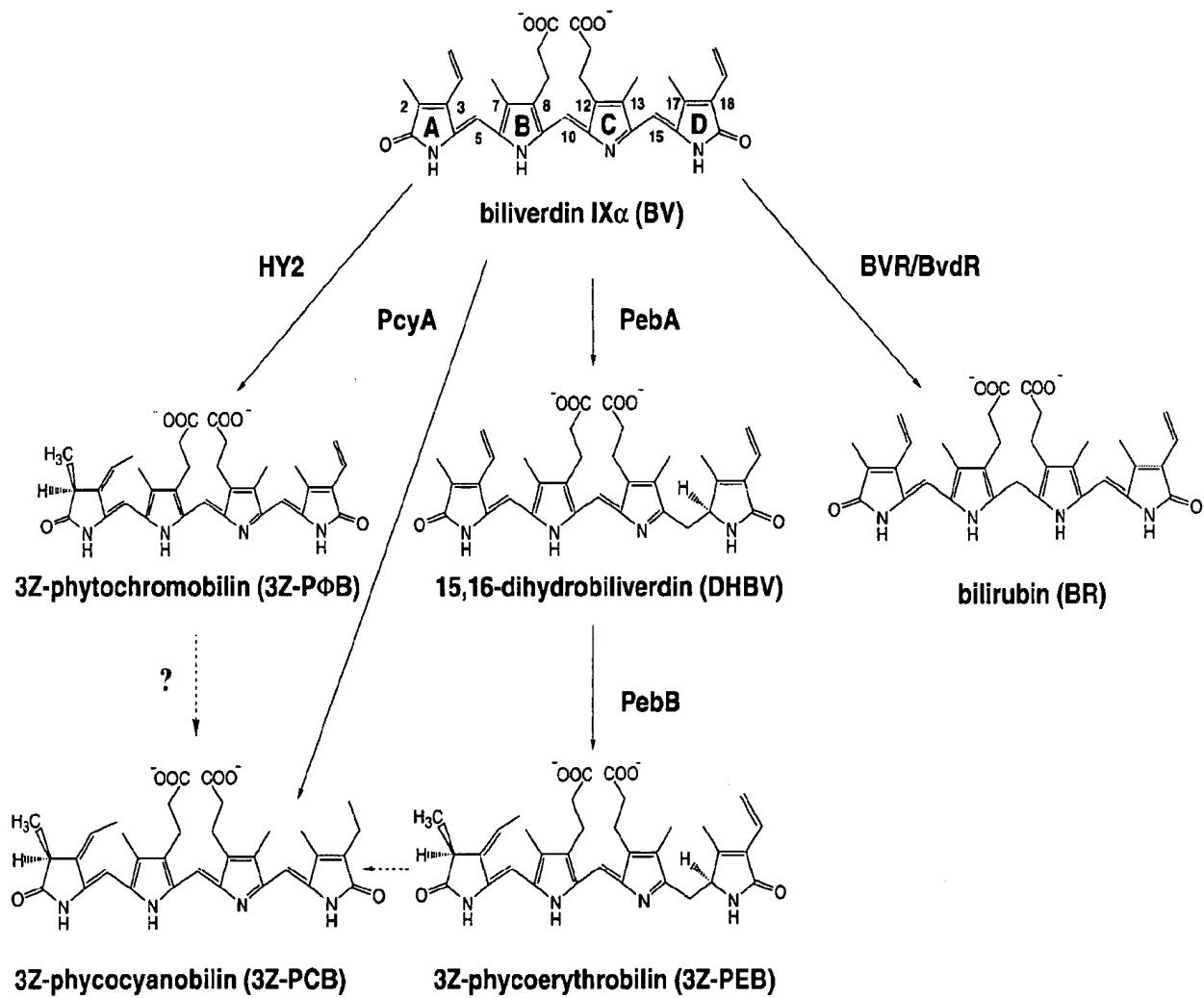


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**Fig. 1**



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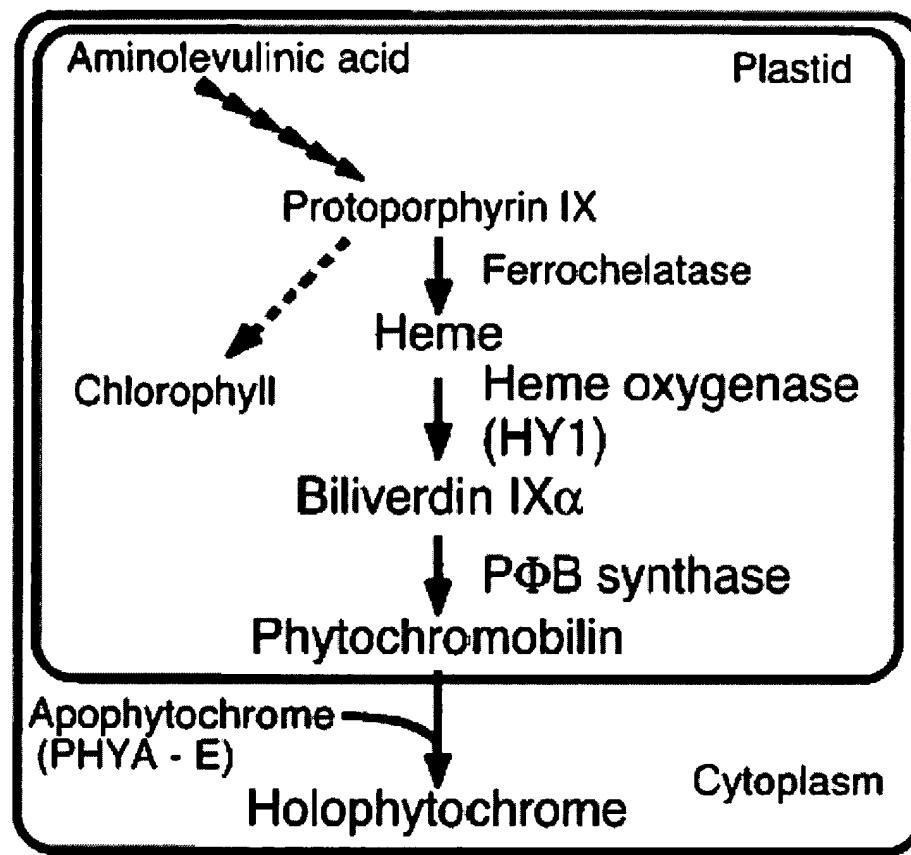


Fig. 2



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gaattccccacgtcaacgtgactgtgcattccacgtggcgatgtggccctatagttgg 60
accatgactcgacggatgttgaattcattgtcggtgcattgcgttgcactga 120
aactgtgaaaattttatcttttataagataaAGAACCTTGCCTTTTCAGTTTCAGTA 180
TGAAGAAGAATTGAAGAGAGTGTCCGAGGAAGGAGACCTTGGTTCAAGTTGTGAGTCT 240
TGTGTAATGGCTTATCAATGGAGTTGGGTTTCAATTGGGTCATGCTCAAGGCACC 300
M A L S M E F G F S I G S C F K A P
AAACCCACCTGTTCTAATCTGCAAGCCCTAATAAGATCAATTTCACGTTGAGAAGGAG 360
N P P V L I S A S P N K I N F T L R R R
AAAGAAAAGATTCTTACTTAGAGTCTGCTGTGCGTATAAGGAATTCCAGAGTCTGC 420
by2-106 *****
K K R F L L R V S A V S Y K E F A E S A
TTTAGAAGAAACCAGGAAAAGGATCGTTCTGAAACCTTCACATCTCCAGgtatatgcaat 480
L E E T R K R I V L E P S H L Q
tacatttcgttagtgttagtggaggattatattctcattgttcttgctgtgaattttg 540
ggtaaaattgatttagttgtcatttaggaaccaaacaataactttactgttataactgc 600
ttatataagtaaaagttcagattttgtttctaatcagaaactgtttcagGAAAAGTA 660
E K Y
TAGTAGCATGACAGGACTAGATGGTAAGACCGAACTTCATAATGCTTGCCTTAAATCTC 720
S S M T G L D G K T E L Q M L A F K S S
AAAGATTAGACTCTGAGGAGTATGGCAATAGAGAACATGCAGgttaacttca 780
K I R L L R S M A I E N E T M Q
gcagtacaaaactgattgttttagtcccatccatttcaattgattgattgttgc 840
by2-105 *****
tcttcgttagGTCTTGTACTTGCCTTCACTGGAGCCTGAGTATGATACTCCATAT 900
by2-1, by2-104 T
V F D F A G F M E P E Y D T P I F
TCTGTGCTAACTTTACATCTACCAACGTTAACATAAGTTGTATTgttaagttatcttct 960
C A N F F T S T N V N I V V L
agttatgtggagttatcaggctgttattgtccaaactgatgtcaatatttactgtat 1020

Fig. 3B



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Fig. 3B cont'd.

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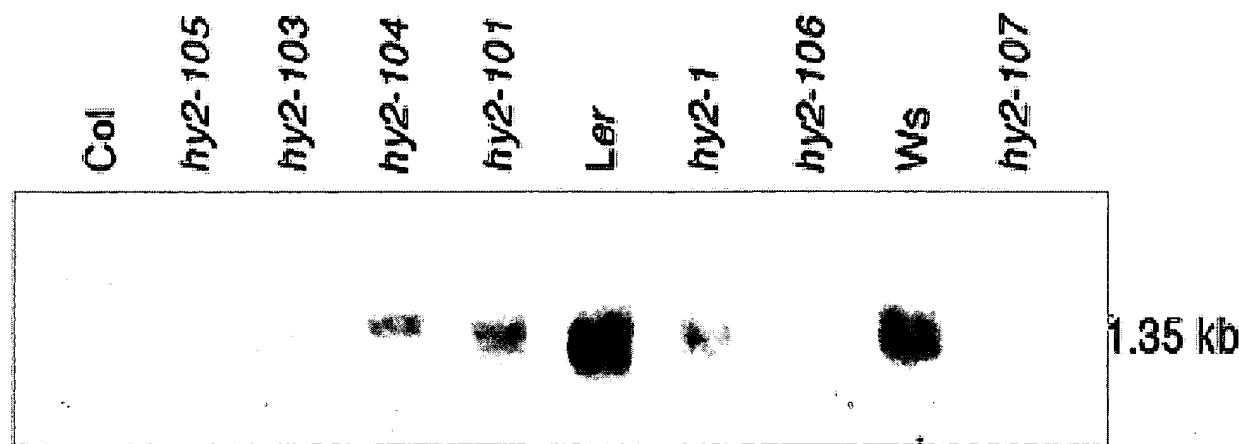


Fig. 4A

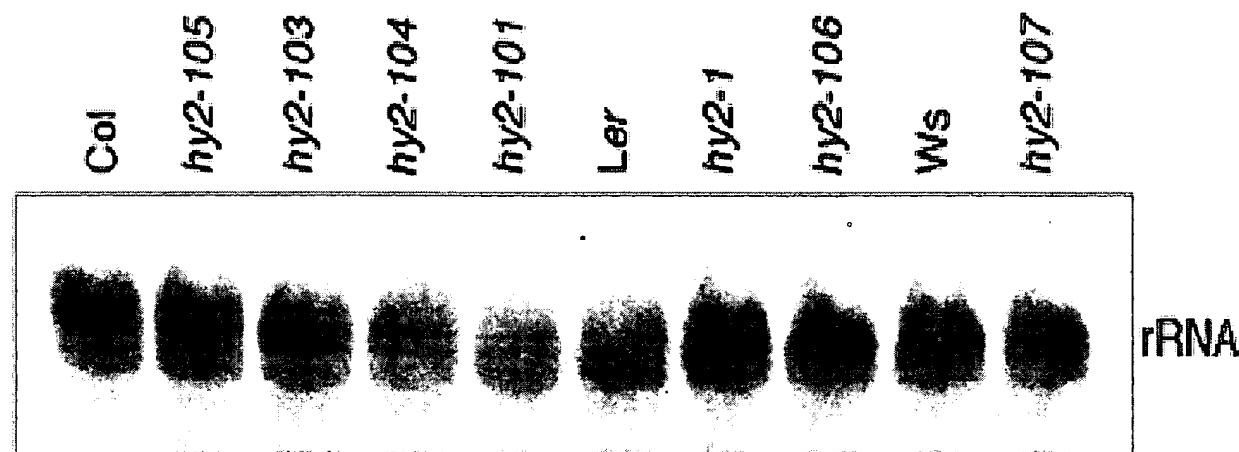


Fig. 4B



09870406 .090402

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	20	40
HY2_ARATH	MAL SMEFGFSIGSCPKA P N P P V L I S A S P N K I N F T L R R R K K	
YCP2_SYNPY	-----	
YHP2_PROMA	-----	
YHP3_PROMA	-----	MI I KRDNS
YCP3_SYNPY	-----	MT N QRFKS
SLR0116	-----	MAVT DLSLTN

	60	80	
RFLLRVS A V S Y K E F A E S A L E E T R K R I V L E P S H E Q E K Y S S M T G L D G K -			86
----- M F D S F L N E L H S D I T K R - - - G G S P L P L P E G L E E C R S S K S S -			36
----- M N K L M L Q D L H N N L K R R I - I S H G G K P I E V E N G M S E R F S H K Q D -			40
LSK I D E R D W I W T P F F N D L V D K L - S V F E I E P Y P V S H D F L S K E S I T G S R			54
T D P V N I E G W S W Q P F L E D A I K R L - E G L N V E S Y P V P D R F L Q R E D Q T G S K			54
S S L M P T L N P M I Q Q L A L A I A A S H - Q S L P L K E Y Q L P E D L G Y V E G R L E G E			56
P 6			

	100	120	
HY2_ARATH	----- T E L Q M L A F K S S K I R L E R S M A T E N - E T M Q V F D F A G E		
YCP2_SYNPY	----- S V I Q S W I W D V P G E R R W R V T R I D A G D S D Q V F N S M A Y		
YHP2_PROMA	----- T V I K S W I W D V P G E R R W R V T R I D A G D K D Q V L N S U A Y		
YHP3_PROMA	----- R N P V H V T T I L T W A A K F E K I K Q V R I A C I K G G E S L S V F N L L I H		
YCP3_SYNPY	----- S K S I P V T T A T W A C K T E K E R Q V R I A C W S A G S A A S V L N F V I N		
SLR0116	----- - K - - L V I E N R C Y Q T P Q E R K M H I E L A K V G K G D I L E C V M F		
4 F 9 6			

	140	160	
ME P E W D T E I F C A N E F T S T N V N - - I V V I L D I N P L H Q L T D Q T D Y Q D K Y M N			165
P D Y N Y D H P L M G V D L I I W F G A R Q K L W A V L D F O P L V Q - - - D K D Y L D R Y E S			115
P A Y T N D K E I I L G I D I I W F G L K R K L W A V L D F O P L V Q - - - E E R Y F C R Y M K			119
P L N D Y D I L P F F G A D F V T L P N G - - H I L A L D I Q P A I K L - - D N I H T E N V W P			137
P K S T Y G L P F F G G D L V T F P A G - - H I L A L D I Q P A I K T - - D E V H T T H V W D			137
P E P L Y G L P L F G C D I V A G P G G - V S A A I A D E S P T Q S - - - D R Q L P A A Y O K			135
P V P g 1 1 D P			

Fig. 5



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180

200

HY2_ARATH	: KTM----S[REDACTED]YHKYAE TF PWGGKLTGES TKFES PLVEM TR
YCP2_SYNPy	: GLK----E INQRE PD LN GEETMRSFD PNQYF SSWLL FCR
YHP2_PRoma	: D EQ ----I IKNRF VD FNSQ KTMKIYDSNK YFSP WVILLYN-
YHP3_PRoma	: R LI ----P LDH W Q SL PSG GEIP KEAE PYF SPG FL MSRL
YCP3_SYNPy	: R LI ----P PER W RD Q LPY GGPIPEEAQ PFF SPG FL W TR
SLR0116	: S LAEL G OP E FE Q QRE L PPW G----E IFSEY C LF I IR

6

FS 6 I

220

240

260

---FSSSKEKKALFSAELEYQANLEETI QVRE EMEP SHVR ANCEA	: 244
---GGAEQADLSLPKAESAE KKAYWD LHDNAKS IP STI P PEEVKNL	: 193
---GSFDDLQCSLAKILDE BLHAYW QDNNNSREYIKIIIPSKV EL	: 197
PLSKESDNII SE ILRPAEGEYLSIYIELLHI AKPLK KER-ALKILEG	: 219
PLGEEGDELIQSIVRPAENDYLDI YLE AAASA ERV TDER-SEVLL OG	: 219
---PSNVTEEERFVQ RVV D EI Q I HCHQSIVAEPL SEAQ -TLEH RG	: 208

51

HY2_ARATH	: QHKYL TWRA OKD E GHGLIKRLVCEAKAKELRDF LE MGVD
YCP2_SYNPy	: QDK DI YSAE RDP A B GLFTSH G KD W S N R F I H E F L E P ASS
YHP2_PRoma	: HIN YD I Y SAE RDP A B GLFKSYFGQ T WADQEVREF LE PHSH
YHP3_PRoma	: QKAY Y IN Y R ST K D PAR A M C REY G K E WT E D Y I H KV L N I --
YCP3_SYNPy	: ORK Y TDYRAE KD PAR G M I TRFH G SE W T E AY I HTV L ED L --
SLR0116	: QIHYC QQQ Q N D K TR Y LEKAEG GE AA A E R Y M S Q V L ED V IQ

q

Y

Dp

6

G

W

6

LF

280

300

ELG T K T F ID Y P PEY Q T E D G T V S D K R S I I G K S Y E T R P W D L T G Q F I G	: 329
SHK----	: 236
LTAD----	: 241
----	: 257
----	: 257
----	: 248

Fig. 5 cont'd.



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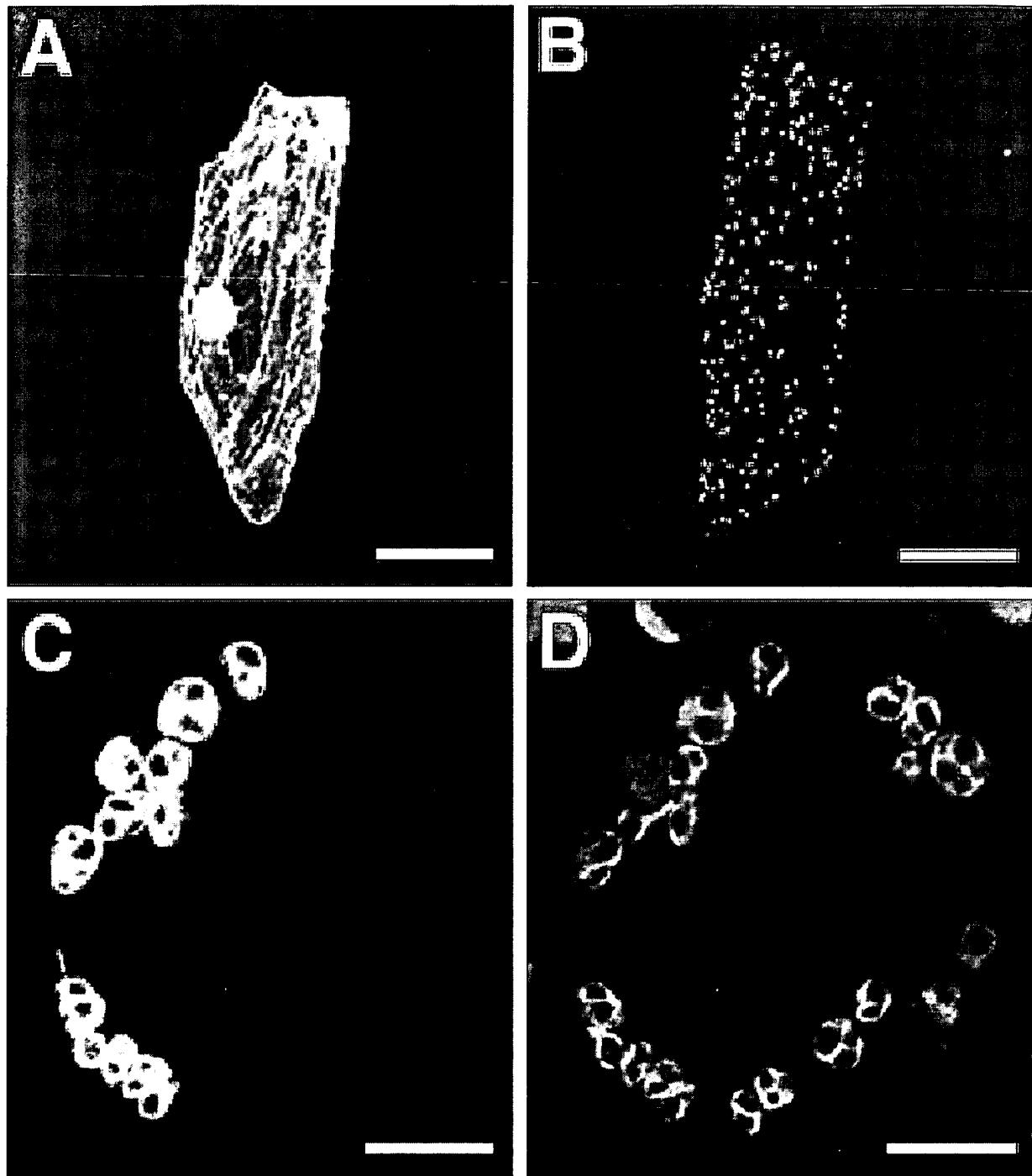


Fig. 6



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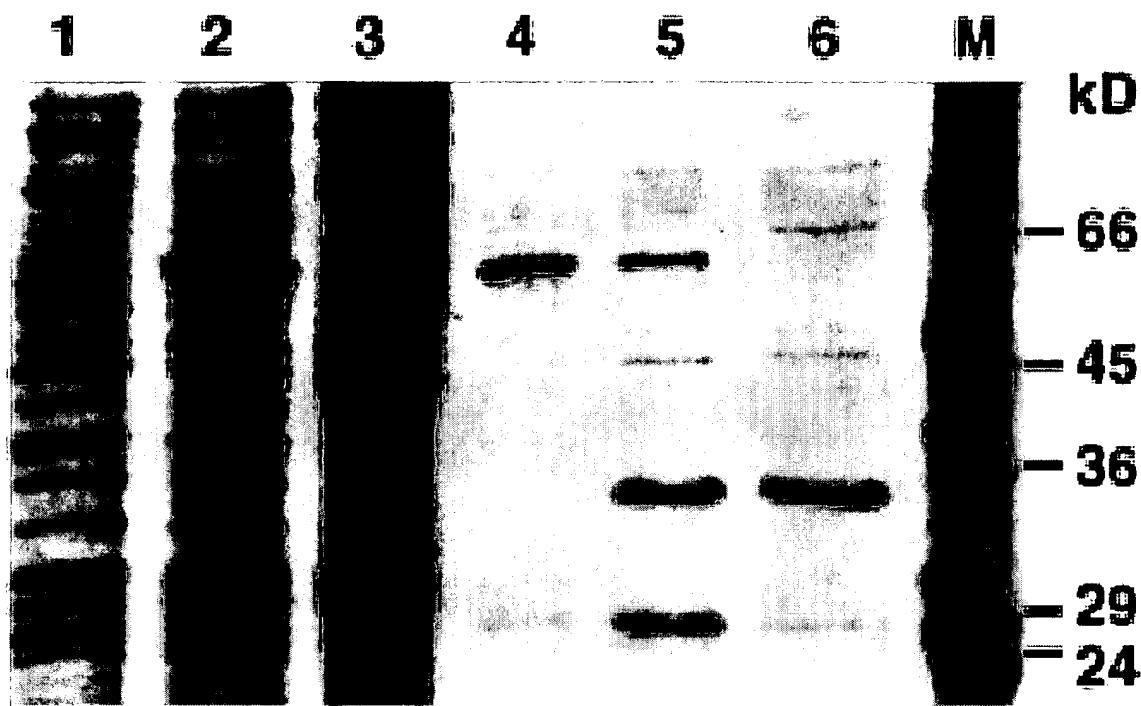
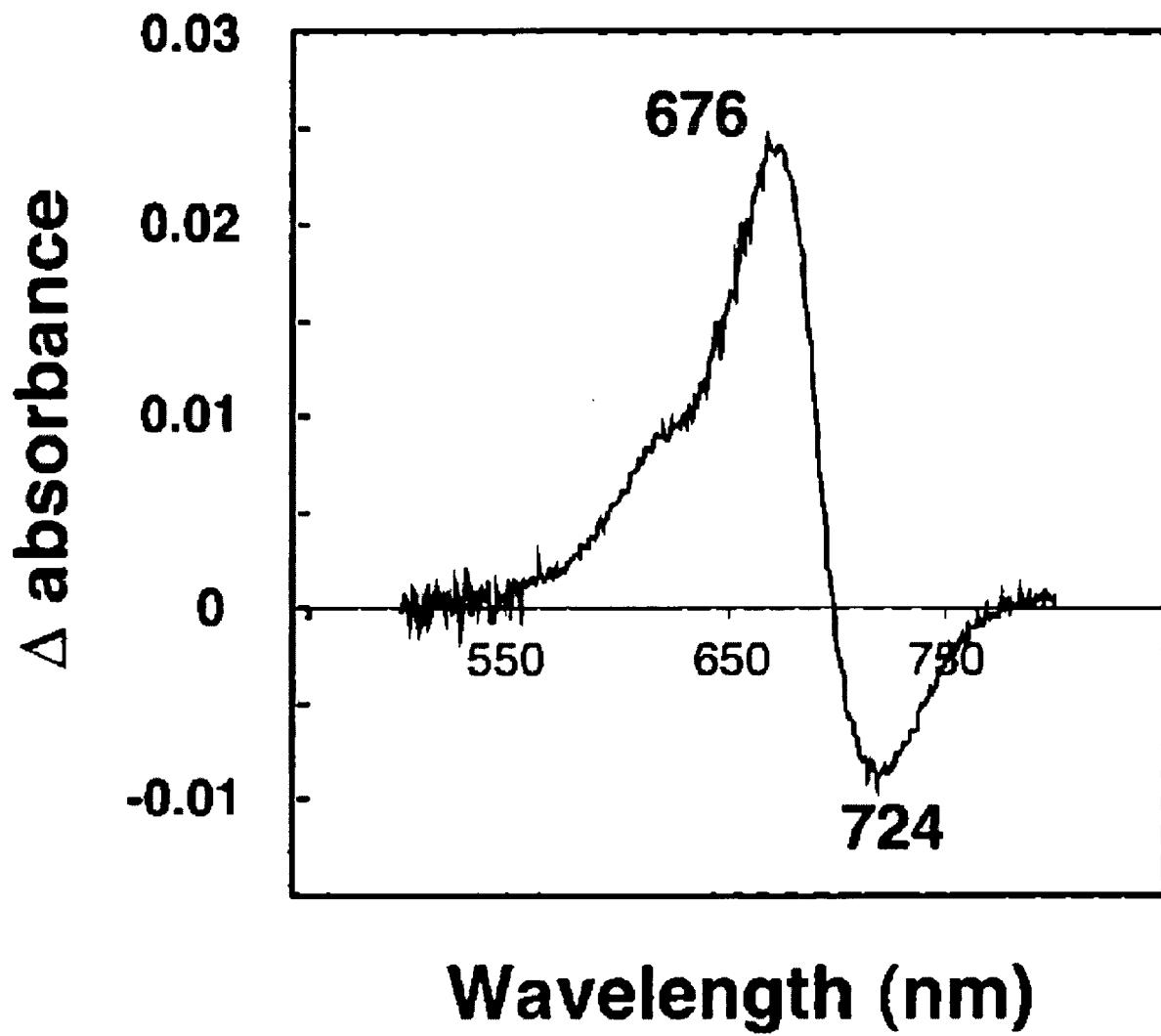


Fig. 7



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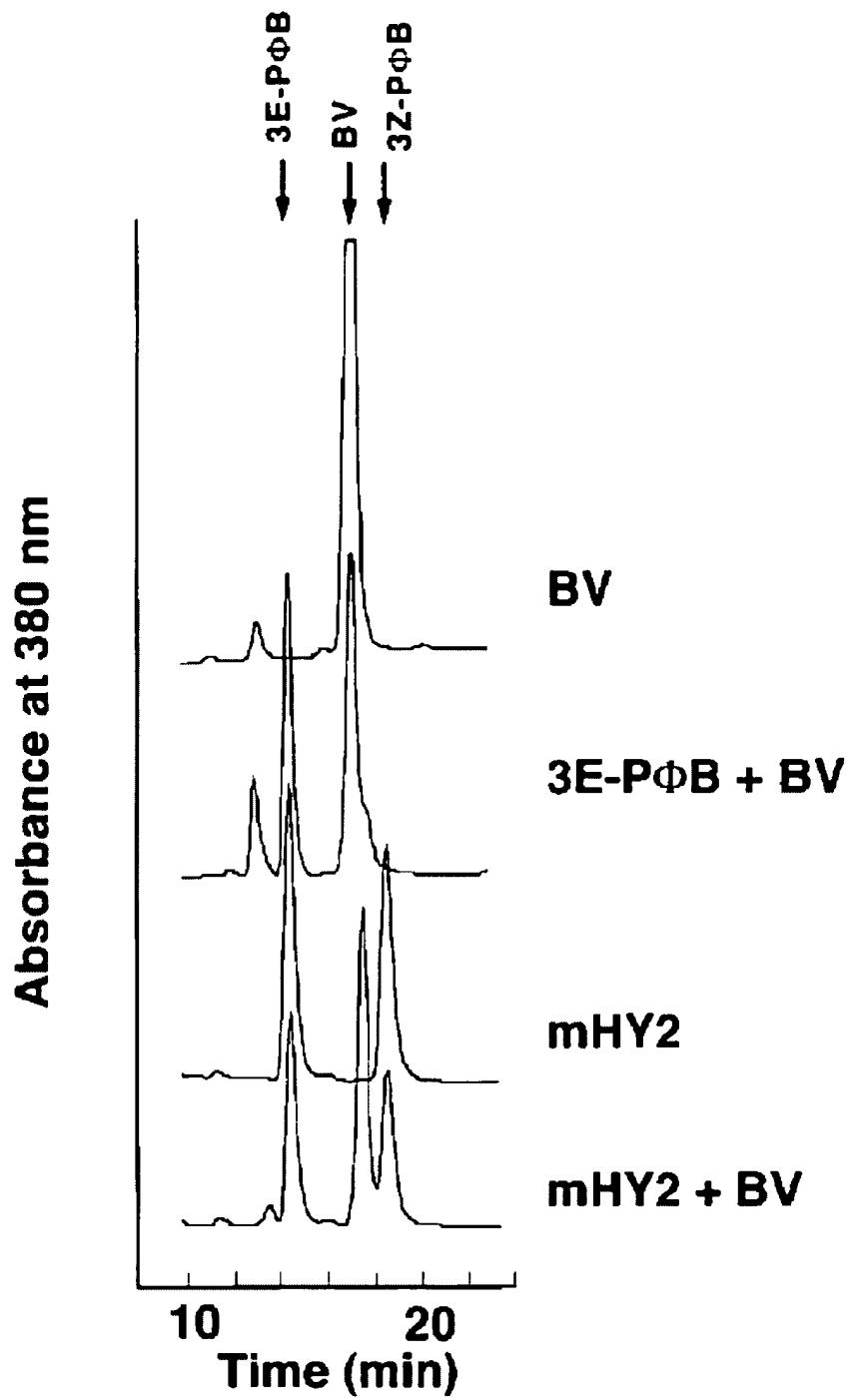


Wavelength (nm)

Fig. 8



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*Fig. 9*



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	* 20 *	* 40 *
PCyA_ANASP :	-----	
PCyA_NOSPU :	-----	
PCyA_SYN3 :	-----	
PCyA_SYN81 :	-----	
PCyA_PROME :	-----	
PebA_SYNPY :	-----	
PebA_SYN81 :	-----	
PebA_PROMA :	-----	
PebA_PROME :	-----	
PebA_NOSPU :	-----	M LN 5 Q S P L R N V A
PebB_SYNPY :	-----	
PebB_SYN81 :	-----	
PebB_PROMA :	-----	
PebB_PROME :	-----	
PebB_NOSPU :	-----	
HY2_ARATH :	-----	M A L S M E F G F S I G S C F K A P N - P P V L I S A
RCCR_ARATH :	M A M I F C N T L Y S S S S P S Y L S P L T S K P S R F S K N L R P R A Q F Q S	
RCCR_HORVU :	-----	

* 60 *	* 80 *	
----- M S L T S I P S L R E Q Q H P L I R Q L A D C H E E V W H Q H L D E S P Y H E P A E L :	43	
----- M S F T S M P S L R E Q Q H P L I R Q L A D C H E A A W H Q H L D E S P Y H E P D E L :	43	
----- M A V T D L S L T N S S L M P T L N P M I Q Q L A L A I A A S W Q S - L P E K P Y Q L P E D L :	46	
----- M Q S P P S E S S S T V A P L I P S L A E T I R G A W I G L P E E K P L D A D S D F :	42	
----- L N L L S K S L T K T K L I D P L I L T L L Q N I K V Q R S K L N D E N C I E V D P K L :	44	
----- M F D S F L N E L H S D I T K - R G G S B L P L P E G L :	27	
----- M F D P F L E E L Q T G I Q A - R G G I S V E W P A G L :	27	
----- M N K L M L Q D L H N N L K R R I I S - H G G K P I E W E N G M :	31	
----- M F E S L K N F V K T N D E - - D E D G K E L E I S K :	25	
I N E T C M I A I T Y F H A R V N K S C S M Y K P F L E F L E K E L F Q R F D E Q S R V I P P G L :	64	
----- M T N Q R F K S T D P V N I E G W S W Q P F L E D A I K R E E G - L N M E B Y P W P D R F :	44	
----- M S I D L R A S S L D P V Q I P G W R W Q P F L D E A S A A D K P - F N P S P Y P I A E T F :	45	
----- M T I K R D M S L S K I D L R D W N T P F F N D L V D K L S V - F E E B Y P W S H D F :	44	
----- M L I Q N T I F Y S Q E W R W A K F I K P L I S Q L D N - Y H C V E H K I A S D F :	40	
----- M N S E R G D V T Y Q P F L D Y A I A Y M R S R L D E E B Y P I P T G F :	37	
K I N F T L R R R K K R F L L R V S A V S Y K E F A E S A L E E T R K R - I V E E P S H L Q E K Y :	77	
H D D H L R R K F M E F P Y V S P T R K Q M V D L M S T V E N R D Q S - - Q E L P C N L P P D V :	90	
-----	-----	

Fig. 10



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	100	* 120 *
PcyA_ANASP	GYVEGRLEGEK-----LT	ENRCYQT PQFRKMHLELAKVG
PcyA_NOSPU	GYVEGRLEGEK-----LT	ENRCYQT PQFRKMHLELANIG
PcyA_SYN13	GYVEGRLEGEK-----LV	IENRCYQT PQFRKMHLELAKVG
PcyA_SYN81	SSIEGQLEGDD-----LL	ERNELLCCRGVRKIHLELARLG
PcyA_PROME	SNIIISNEBGKE-----LY	TENEFYAKGFRKLHIBVAEFS
PebA_SYN14	EECRSSKSS-----SVI	QSWLWDV PGFRRWVTRLDAG
PebA_SYN81	EHNQSQKGS-----STI	QSWLWQV PGFRRWVTRLDAG
PebA_PROMA	SERFSHKQD-----TVI	KSWLWDV PGFRRWVTRMDAG
PebA_PROME	EFKEHHNKD-----SKY	IIKNWIEESQQYRKWRITKLIDGG
PebA_NOSPU	EFKVSDRGR-----NPAT	IRSVCYQSQELRKIRYTYIDAG
PebB_SYN14	LQREDQTGSKSK-SIPVTT	ATWACKTEKFQURAACVSAG
PebB_SYN81	LQKEGSTGSKAK-PVPVTT	ATWACSTDQLRQVRCAACVEAG
PebB_PROMA	LSKESITGSRRN-PVHVTT	LTWAAKFEKIQURLACIKGE
PebB_PROME	SYKESSYGSKKSKKNIN	FTWGATHQKRINFARAVCINS
PebB_NOSPU	ESNSAVVGKGKN-QEEVVT	TSYABQTAKLQDRAAHVQGE
HY2_ARATH	SSMTGLDG-----KTE	QLMLAEKS SKIRLRSMAIEN-
RCCE_ARATH	RNFNNPNGSAEASLHI	RSGDKSSPIDFVIGSWIHCKIPTG
RCCR_HORVU	-----	-MDFNLQSSLHCKUPNG

	140	*	160	*	180	
NMLD	DLHCVMFFPRPEYDLPMEGCDLVGGR-GQISAAEADLSFVHL---DRTL					: 126
NMLO	DLHCVMFFPRQYNEPMEGCDLVGGR-GQISAAEADLSFVQL---ERTL					: 126
KGLD	DLHCVMFFPEPLYGLPREGCDIVAGP-GGVSAAIADLSPTQS---DRLQ					: 129
RGLD	DLHCVMFFPDPRFDLPIEGADIVAGP-AGVSAAIIVDLSPVV---SGTL					: 123
IKSLK	DLHCVMFFPDPKYDTPPIEGMDIVKVN-ELVSAAIIVDLSPSK---NQNL					: 127
DSLOV	ENSVAYPDYNYDHPMGVDLLWFGARQKLQAVLDFQPEEVQ---DKDY					: 109
DSLOV	ENSVAYPDFDLDHPMGVDLLWFGARQKLQAVLDFQPEEVQ---DKDY					: 109
DKLOV	ENSVAYPAYTNDKPDLGIDLWFGLKRKLVAVLDFQPEEVQ---EERY					: 113
DKLOV	FNTVAYPNFKSEFPILGADLWFEGTSQKLLAIFDQYQPEBIQ---EKKY					: 109
ESAOQ	IFNSVYVPSHNYDQPELGIIDFLSFG-KVKNLIVLDFQPEFQ---DEDY					: 147
SAASV	ENFVINPKSTYGLPREGGDIVTFP---AGHLLALDQPAIK---TDEVH					: 131
MAASV	ENFVINPSCRFDLPPREGADIVTLP---NGHLLALDQPVDK---ADPDH					: 132
ESTB	WVNLLIHPLNDYQEPFREGADFTLP---NGHLLALDQPALK---LONIH					: 131
PNYSV	ENFLIIPKTSYNIPELGUDFJSLP---TSHLLVLDQPSLK---VENQF					: 127
INSLQV	ENFVIFPHLNYYDQPEFREGADIVTLP---GGHLIAALDQPFFR---DOSAY					: 124
ETHQV	FDFAGEMEPEYDTPIERCANFTST---NVNIIVLDENPQHQLTDQTDY					: 159
VSLN	WITSISGFLNSSTKAPNEVVELIQQSS-SKS LVLILDEPHRKDLVLPDY					: 181
-AID	ITSLFINLNASTDAPHEIMEFIQGS-PTSMWJLLDLERKDLALHPEY					: 66

Fig. 10 cont'd.



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	200	*	220
PcyA_ANASP	PESYNSAITSINT---	LNFSQPRELPWGNI	FSDF
PcyA_NOSPU	PESYTTALAQLPV---	LNFSQPRELPWGNI	FSDF
PcyA_SYN3	PAAWQKSIAELGQ---	PEFBQQRELPPWGEI	FSBY
PcyA_SYN81	PSGIETALAGTPS---	PAFRQVRDLPWGWTI	FSBH
PcyA_PROM	--KVDHLLSHIDK---	SVFKSKREIPIWGNI	FSKN
PebA_SYNPY	LDRYFSGIKELNQRF	PDLNGEETMRSFEPNQY	FSSW
PebA_SYN81	LDRHFDGLKDLNARF	PDLNGEETMRSFEPNQY	FSSW
PebA_PROMA	FCRYYKDIQIIKNRFVDF	NSQKTMKIYDSNKY	FSPW
PebA_PROM	LOKYCSSUDFTKNOY	SVDNHKMKNIYDSKKY	FSPW
PebA_NOSPU	QNKYIAPIKYLHINKY	PDLAQNLLEMKFYDANQY	FSKY
PebB_SYNPY	THVWDRLLTPIFERWRDQL	PYGGPIPEAQPF	FSPG
PebB_SYN81	TQFVWERLMPLFERWQAE	LPDGGPIPEAQPF	FSBA
PebB_PROMA	TENVWPRLLTPIFHLDHWQ	SLLPSGGEIPKEAEPY	FSPG
PebB_PROM	NSELLEQIIKIKLKSCH	SSLPVAEKMSEIVAKF	FSPG
PebB_NOSPU	QAKYTEPILPIFHAAHQQL	SWGDFPEAQPF	FSPA
HY2_ARATH	QDKYMYNKIMSIYHKY	AETFPWGGKLTGESIKF	FSPL
RCGR_ARATH	LKEVYQDTALDSHRQ	SLLKLPEVNPYVSPSLFVRSA	FSNT
RCCE_HORVU	IEKYYEDTEVDKQRKII	EQLPQARPYLSPSLFVRSA	FSPT

4

FS

	240	*	260	*					
CIFVRP-----	SSPSEEAMFLGRVREFI	QVHCQGAIAA	SPVSAEOK	: 199					
CIFVRP-----	GSPSEEAMFLSRVREFI	DQHCMQAIA	HPVSVEQV	: 199					
CIFIRP-----	SNVTEEERFVQRVVD	FLQHCHQSIV	EPLSEAQT	: 202					
IVCFIRP-----	DGAEEEVLFRSRVEE	VLTFLRTAVL	QTAECPATAAST	: 198					
MFEASL-----	KNESEKNAFCKIVDN	YLSVLIQLSQST	SPDSDYEI	: 198					
ILFCRG-----	GAEQADLSLPKA	FSAFIKA	WDLH DNA	KSIPSTIP	: 186				
ILFCRG-----	GSEADRS	LPKA	FSAFIKA	WGLHDEA	-SKEPSIS	: 186			
MILYNG-----	SPDDLQCSLAK	ILDEFIHA	WQVDNNN	-SR EYIKII	: 190				
VMICRG-----	NKLNLDRDLNN	IFCSFVSNVLT	TINKLH	-ONNOFLD	: 185				
LLFAKT-----	DAETVSTRVFEAFQDY	IN	WQMLADA	-QAEHD PED	: 224				
FLWTRIPLGE---	EGDELIQSI	VRPAFNDY	LDL	YLELAASA	-ERVTDERS	: 213			
FLWTRIPLGE---	EGDELI	ERVPAFIDY	LQ	YLN LVA	EEFVSD DRA	: 214			
FLUSRLPLSK---	ESDNII	SEILRPAFCEY	YLS	LYTELLHIA	-KPEKKERA	: 213			
ILINSRLAKHQ---	DSDNLIENQL	IDSFKEY	YIN	BLVKT	L FES	-EEVMGHGLQ	: 209		
FLINTRP-----	QETAVVETQVFAA	EFDY	LKAYLDF	VEQA	-EAVTDSQN	: 202			
VMNTRF-----	SSSKEKH	KALFSAF	LEY	YQAWLEM	TIQV	--REEMEP SH	: 237		
ASMLKIDABE	EDKLE	EILRDH	VSPA	AAKEV	IDE	WLERCVKE	EE EK	IVVGE	: 271
AVFTIDCGKG	EGTLE	EIVHGH	LASVVKG	I	LOQ	DWLDTCA	SD	--ASEMEEG	: 155

4

Fig. 10 cont'd.



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	280	*	300	*
PcyA_ANASP	QQILIA-GOHNYC SKOOOND KTR RUE EK F GUDTAEN YMTT			
PcyA_NOSPU	TQNLIA-GOHNYC TKQQQND KTR RUE EK F GPVWAEN YMTT			
PcyA_SYN3	LEHRQ-GOIHYC QQQQKND KTR RUE EK F GEAWAER WMSQ			
PcyA_SYN81	IRR YE-GOLSYC LQQ KRN D KTR RUE EK F DASHAER YIKE			
PcyA_PROME	IEERIMYCKNYC VQOMKNE KTS L VELRY F DKVUVVDE YIKK			
PebA_SYNPY	PEEWKWLQDKYD IYSAERD PAHGLFTSHEGKEMSNRFLHE			
PebA_SYN81	PGDWERLQNAVYD VYSAERD PAHGLFTSHEGKEMSNRFLHE			
PebA_PRAMA	PSKWEQLHINYD IYSAERD PAHGLFKSY F GQTWAQF VURE			
PebA_PROME	LEQIKNNQIDYD KYSAEKD RADKLFKTF F GETWTEN SINN			
PebA_NOSPU	IQRIVKAQDKYD QYSAERD PASGLFSSY F GHEWAER ELHE			
PebB_SYNPY	EVLLQ-GORKYT DYRAEKD PARGMUTRFHGBEWTEA WIHT			
PebB_SYN81	ELLS-GOKRYTA YRAEKD PARGMUTRFYGS EWT ESYIKG			
PebB_PRAMA	LKILE-GOKAYIIN YRSTK D PARMACRFY GKEWTE D YIKK			
PebB_PROME	QELIN-GQNDYLN YR RDND D PAR PMLS SLECKDFTESLINK			
PebB_NOSPU	LVAIKQAOLRYL RYRAEKD PARGMFKRFYGAEWTE EYIKG			
HY2_ARATH	VRANCEAOKYL TWRAQKD PGHGLKRLVGEAKAKELLRD			
RCCR_ARATH	ERMELER RDKSF RRSK SIE D DLDLQF PRME GEEVSSR VVHA			
RCCR_HORVU	ERETMVKDRD TVRSKSIEVDLTANL PRME GPDVSGRIIAE			
	Q	Y	1	4
			3G	4

	320	*	340	*	360	
VLFDLPE	-----		-----		-----	: 245
VLFDLPT	-----		-----		-----	: 245
VLFDVIQ	-----		-----		-----	: 248
VLFDODPLPPG	-----		-----		-----	: 247
VLFDL	-----		-----		-----	: 243
VLFPASSSHK	-----		-----		-----	: 236
VLFPASQPA	-----		-----		-----	: 235
VLFPHSHTAD	-----		-----		-----	: 241
VLFLNHNPLK	-----		-----		-----	: 236
VLFEDAVPLAVSASKR	-----		-----		-----	: 280
VLFDL	-----		-----		-----	: 257
VLFDLEDAA	-----		-----		-----	: 262
VLFENI	-----		-----		-----	: 257
VLFSTTNKVL	-----		-----		-----	: 257
VLFDLERKLTVVK	-----		-----		-----	: 255
VLENGVDELGTKTFIDYFPEYQTE DGT VSDKRS IIGKSY ETR PWDL TGQFIG	-----		-----		-----	: 329
IKKEAFGVL	-----		-----		-----	: 319
IRKAFGVQEG	-----		-----		-----	: 205
LP						

Fig. 10 cont'd.



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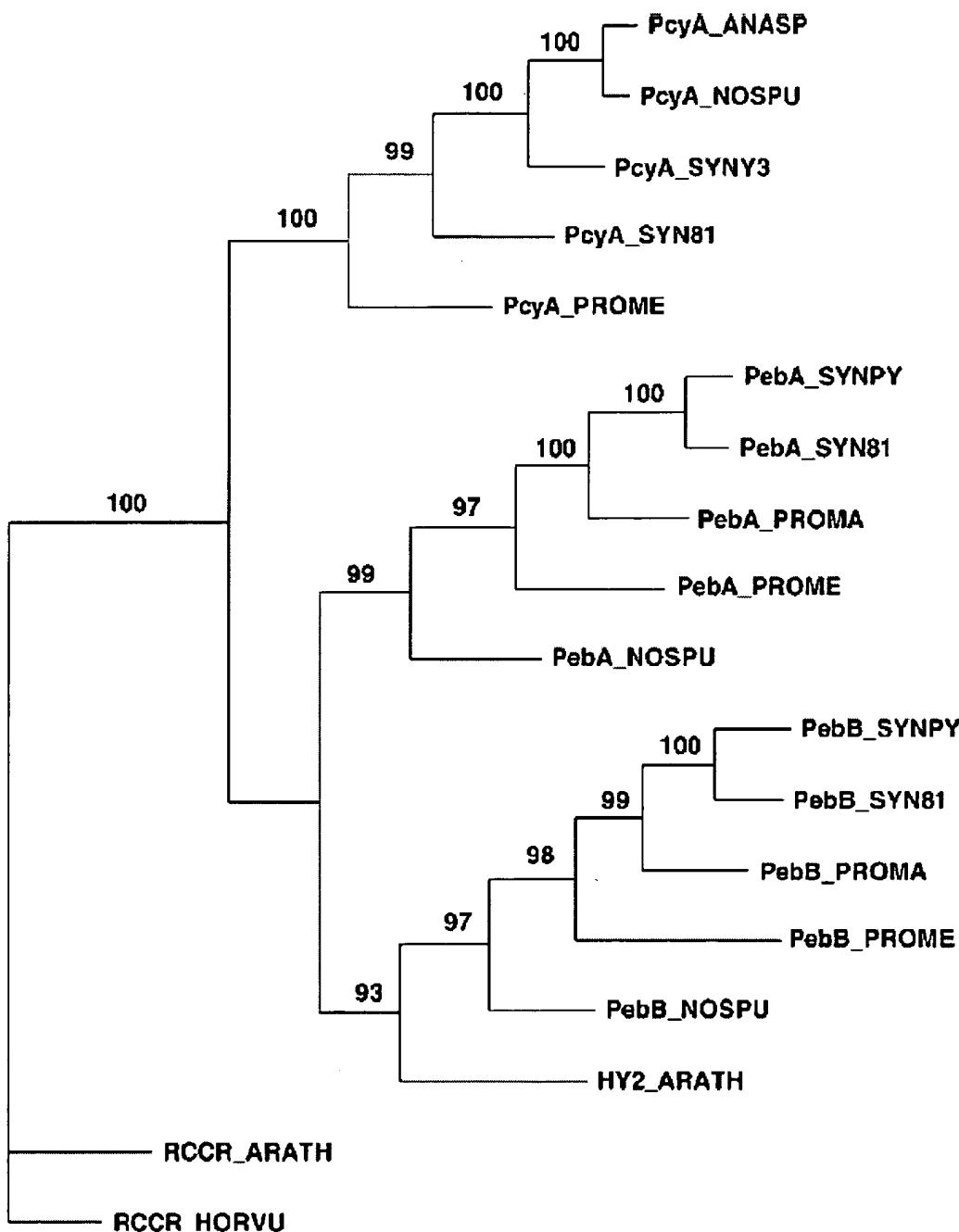
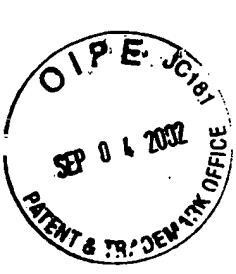


Fig. 11



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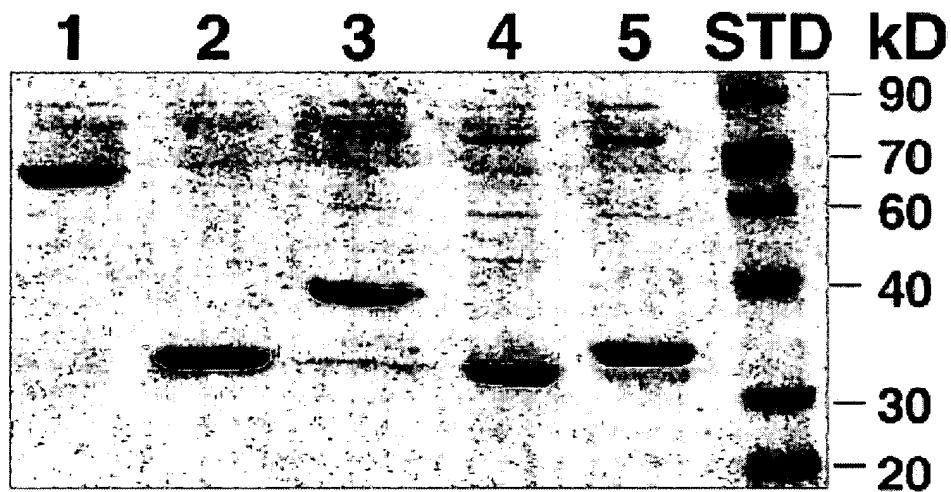


Fig. 12



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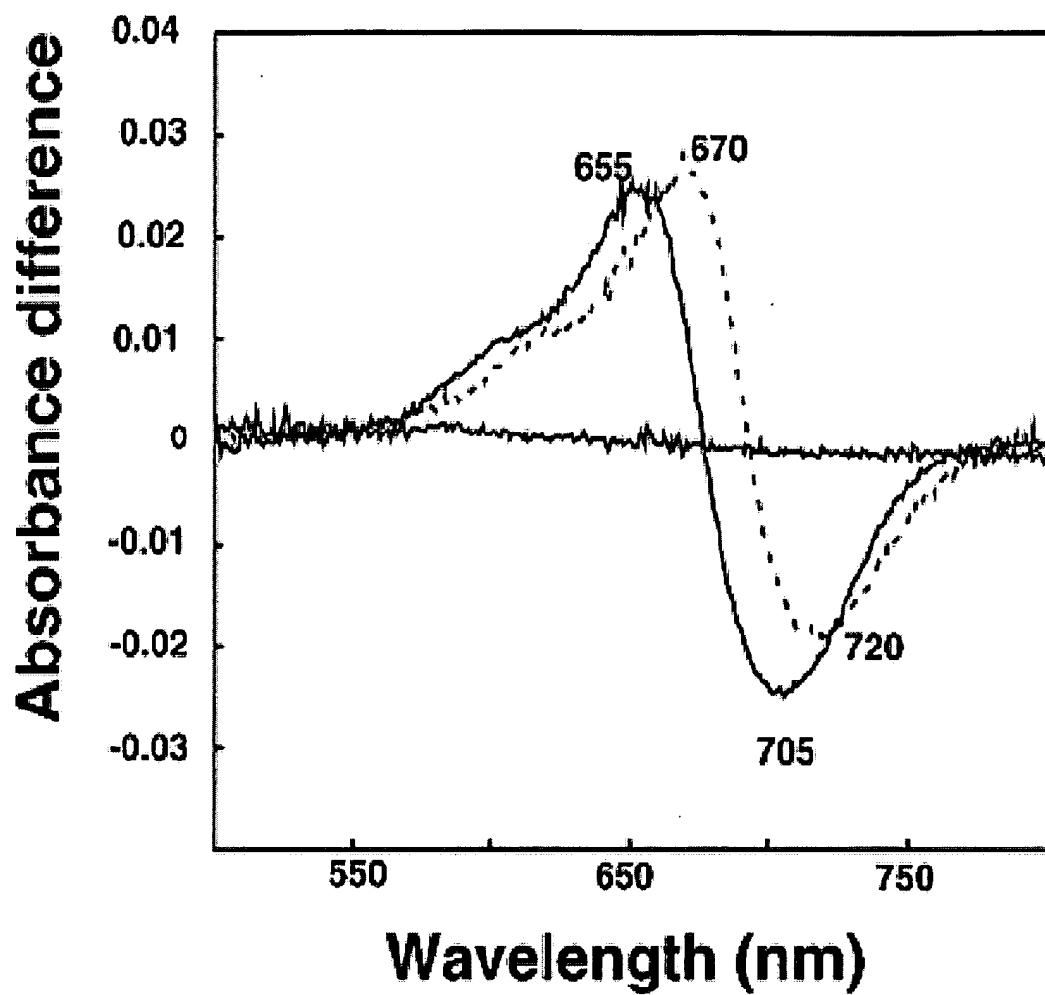


Fig. 13A

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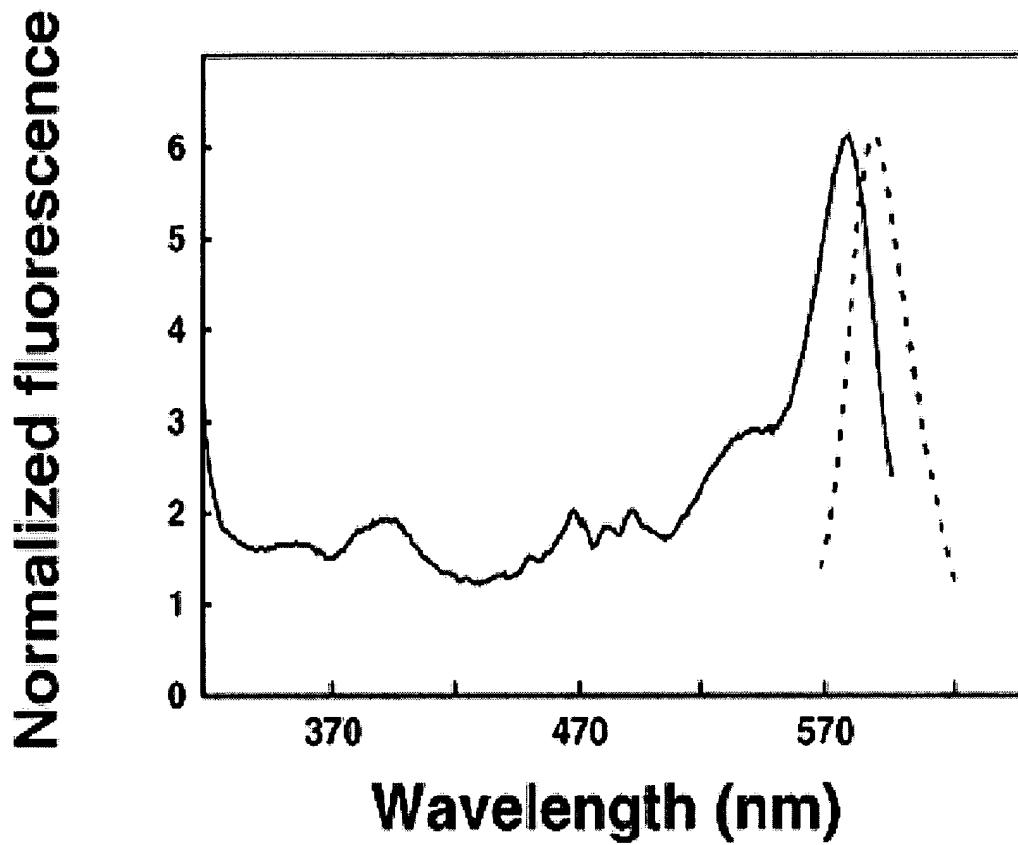


Fig. 13B



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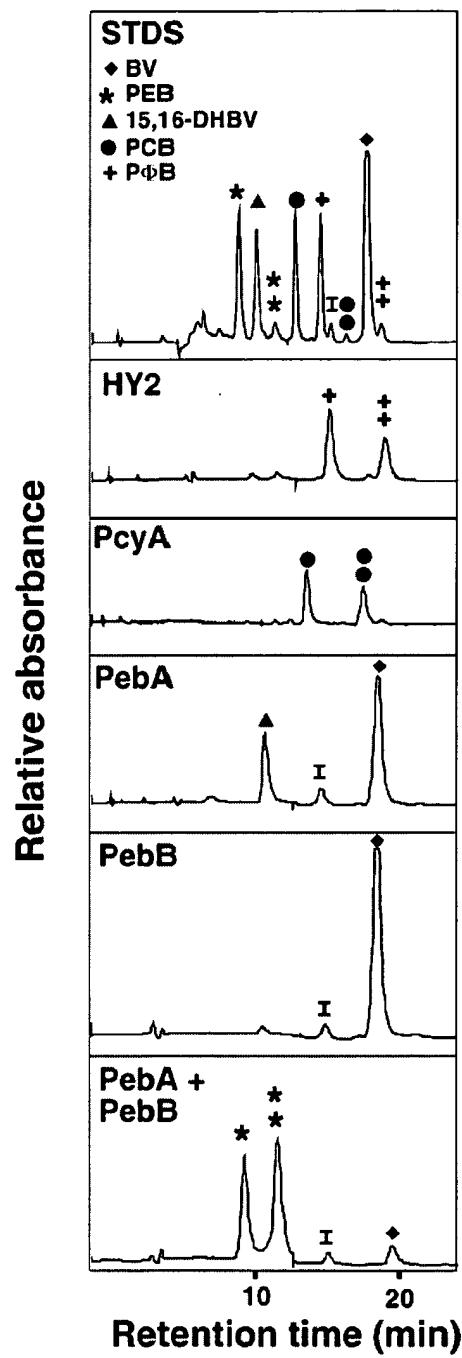


Fig. 14



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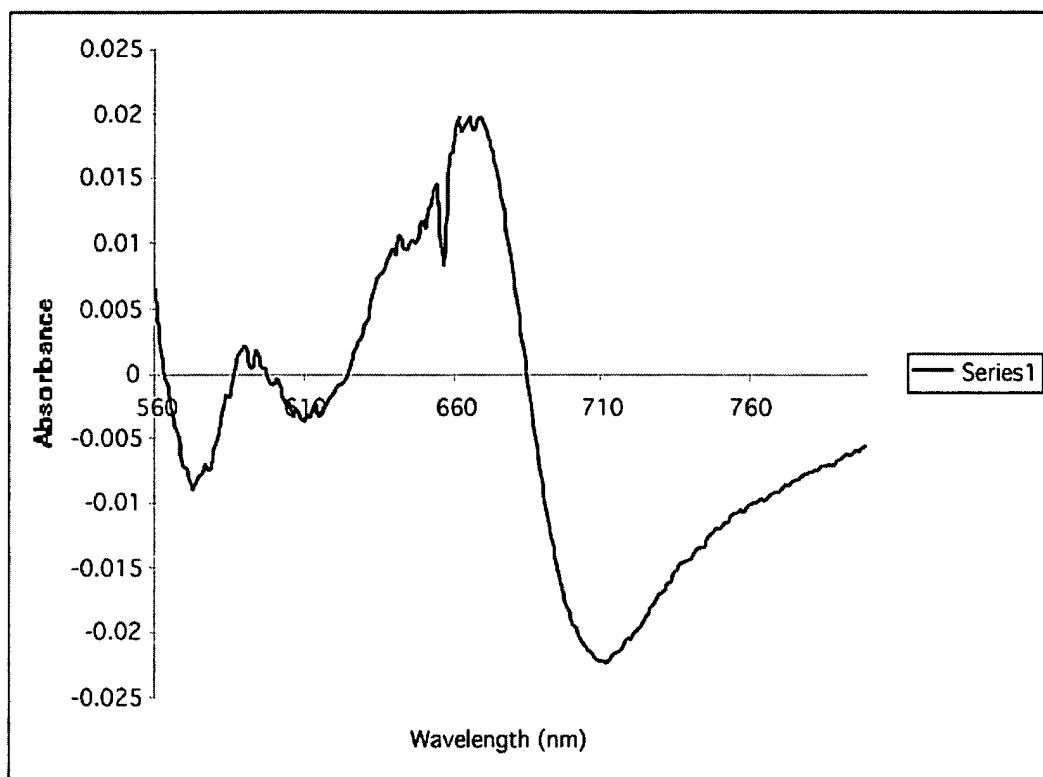


Fig. 15



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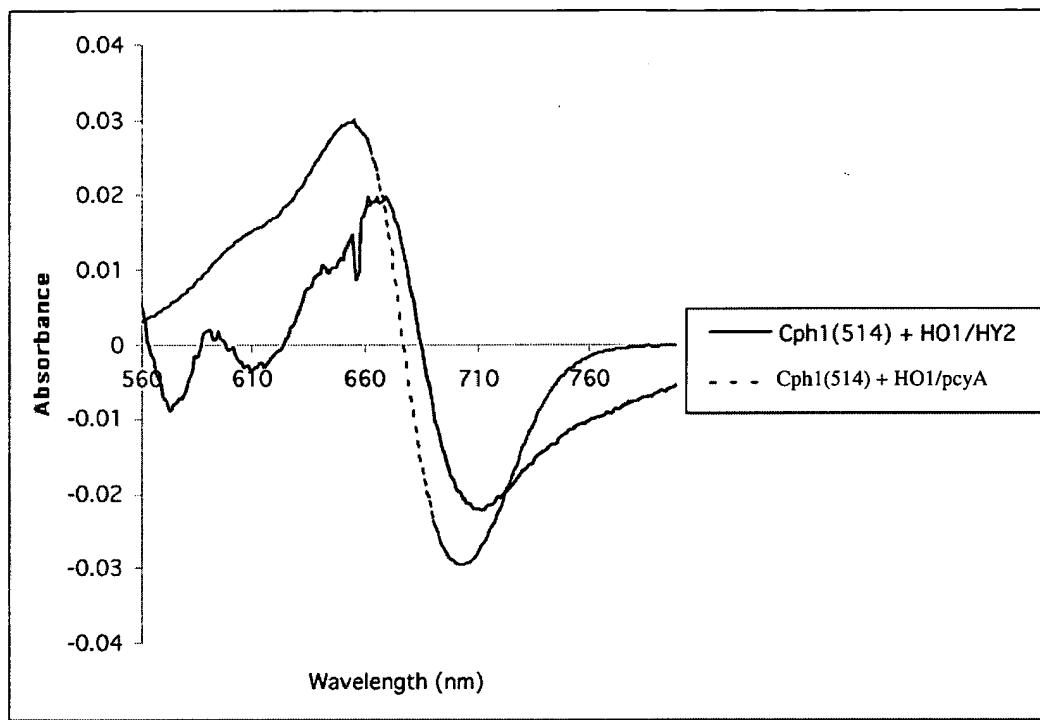


Fig. 16